

036/0590



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RAW SEQUENCE LISTING

DATE: 03/06/2002

PATENT APPLICATION: US/09/944,049

TIME: 13:04:54

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Output Set: N:\CRF3\03062002\I944049.raw

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3 <110> APPLICANT: Schall, Thomas J.
4   Penfold, Mark E.T.
5   ChemoCentryx, Inc.
7 <120> TITLE OF INVENTION: Inhibition of CMV Infection and Dissemination
9 <130> FILE REFERENCE: 019934-002510US
11 <140> CURRENT APPLICATION NUMBER: US 09/944,049
12 <141> CURRENT FILING DATE: 2001-08-30
14 <150> PRIOR APPLICATION NUMBER: US 60/229,365
15 <151> PRIOR FILING DATE: 2000-08-30
17 <160> NUMBER OF SEQ ID NOS: 48
19 <170> SOFTWARE: PatentIn Ver. 2.1
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22 <211> LENGTH: 1065
23 <212> TYPE: DNA
24 <213> ORGANISM: Human cytomegalovirus
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28   reading frame US28 (AU4.1)
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
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33 <223> OTHER INFORMATION: HCMV Toledo US28
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38 ggcgttggtct ttctgttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
39 cgacgtcgga ttcaatgctc cggcgatggt tactttatca acctcgcggc cgccgatttg 240
40 cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacia ctccctagcc 300
41 agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgtgt 360
42 tttatcacgg agattgcact cgatcgctac tacgctattg tttacatgag atatcggcct 420
43 gtaaaacagg cctgcctttt cagtattttt tgggtgatct ttgccgtgat catcgccatt 480
44 ccacatttta tgggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
45 gaggtcagct acccgatcat cctcaacgta gaactcatgc tcggtgcttt cgtgatcccg 600
46 ctcaagtgtca tcagctactg ctactaccgc atttccagaa tcgttgccgt gtctcagtcg 660
47 cgccacaaag gtcgcattgt acgggtactt atagcggctg tgcttgtctt tatcatcttt 720
48 tggctgccgt accacctaac gctgtttgtg gacacgttaa aactcctcaa atggatctcc 780
49 agcagctgcg agttcgaaa atcgctcaaa cgtgcgctca tcttgaccga gtcgctcgcc 840
50 ttttgtcact gttgtctcaa tccgctgctg tacgtcttcg tgggcaccaa gtttcggcaa 900
51 gaactgcact gtctgctggc cgagtttcgc cagegactct tttcccgcga tgtatcctgg 960
52 taccacagca tgagcttttc gcgtcggagc tcgccgagcc gaagagagac atcttccgac 1020
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56 <210> SEQ ID NO: 2
57 <211> LENGTH: 354

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58 <212> TYPE: PRT
59 <213> ORGANISM: Human cytomegalovirus
61 <220> FEATURE:
62 <223> OTHER INFORMATION: human cytomegalovirus (HCMV) Toledo strain open
63   reading frame US28 (AU4.1)
65 <400> SEQUENCE: 2
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69 Asp Glu Ala Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
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72 Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
73   35           40           45
75 Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
76   50           55           60
78 Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Asp Leu
79   65           70           75           80
81 Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
82           85           90           95
84 Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
85           100          105          110
87 Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
88           115          120          125
90 Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
91           130          135          140
93 Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
94           145          150          155          160
96 Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
97           165          170          175
99 Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
100          180          185          190
102 Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
103          195          200          205
105 Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
106          210          215          220
108 Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
109           225          230          235          240
111 Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
112           245          250          255
114 Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
115           260          265          270
117 Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
118           275          280          285
120 Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
121           290          295          300
123 Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
124           305          310          315          320
126 Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
127           325          330          335
129 Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile

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142     reading frame US28
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (1)..(1065)
147 <223> OTHER INFORMATION: HCMV VHL/E US28
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151 actccctgtg tcctcaccga cgtgcttaat cagtcgaagc cagtcacggt gtttctgtac 120
152 ggcgttgtct ttctcttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
153 cgacgtcgga ttcaatgttc cggcgatgtt tactttatca acctcgcggc cgccgatttg 240
154 cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacia ctccctagcc 300
155 agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgtgt 360
156 tttatcacgg agattgcact cgatcgctac tacgtatttg tttacatgag atatcggcct 420
157 gtaaaacagg cctgcctttt cagtattttt tgggtggatct ttgccgtgat catcgccatt 480
158 ccacacttta tgggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
159 gaggtcagtt acccgatcat cctcaacgta gaactcatgc tcggtgcttt cgtgatcccg 600
160 ctcagtgtea tcagctactg ctactaccgc atttccagaa tcggtgcggg gtctcagtcg 660
161 cgccacaaaag gccgcattgt acgggtactt atagcggtcg tgcttgtctt tatcatcttt 720
162 tggctgccgt accacctgac gctgtttgtg gacacgttga aactgctcaa atggatctcc 780
163 agcagctgcg agttcgaaaa atcactcaag cgcgcgtca tcttgaccga gtcactcgcc 840
164 ttttgtcact gttgtctcaa tccgctgctg tacgtcttcg tgggcaccaa gtttcggcaa 900
165 gaactgcaact gtctgctggc cgagtttcgc cagcgactgt tttcccgcga tgtatcctgg 960
166 taccacagca tgagcttttc gcgtcggagc tcgccgagcc gaagagagac gtcttcgcag 1020
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177     reading frame US28
179 <400> SEQUENCE: 4
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181 1 5 10 15
183 Asp Asp Glu Ala Thr Pro Cys Val Leu Thr Asp Val Leu Asn Gln Ser
184 20 25 30
186 Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
187 35 40 45
189 Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
190 50 55 60
192 Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu

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193 65          70          75          80
195 Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
196          85          90          95
198 Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
199          100          105          110
201 Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
202          115          120          125
204 Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
205          130          135          140
207 Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
208 145          150          155          160
210 Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
211          165          170          175
213 Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
214          180          185          190
216 Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
217          195          200          205
219 Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
220          210          215          220
222 Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
223 225          230          235          240
225 Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
226          245          250          255
228 Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Lys Ser Leu Lys Arg Ala
229          260          265          270
231 Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
232          275          280          285
234 Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
235          290          295          300
237 Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
238 305          310          315          320
240 Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
241          325          330          335
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258 <220> FEATURE:
259 <221> NAME/KEY: CDS
260 <222> LOCATION: (1)..(1020)
261 <223> OTHER INFORMATION: rhUS28.1
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265 atagctattg ctatgtacag cattgtttatc tgtatcgggt tgggttgaaa cctgctgtta 120
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267 gcctctatgg ccgacctgt cagcaactgt atgctaccgc tctggctaca ttatgtctc 240
268 aactttgccc aactctctcg aggagcctgt atcagctttt cgggtgacttt ctatgttccc 300
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271 tctgccttcg tggcatcacc ctactacgca tacagaaact cacacgacga acacgaatgc 480
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273 atcatagtat ggaccttttt ggccccagta ctggtaacca ttatagcaag cgtcaaatg 600
274 agacgaacga cctggggcaa tactaggtta aacgaaaaga acagcgacat tcttatagta 660
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276 attttacaga gatactatga taccacgaat tgcgatgtag aaaagattaa acatatcatg 780
277 gctatgatct cagaagccat tgtttatttt cgcggtatta cagcacctat tatttatgta 840
278 gggattagtg gcagatttcg cgaagagatt tactctctgt ttagacgcca gccgtataac 900
279 gatttggacc ccgatgcaa tcaattcatg attgaactca ctagccaggg aagaagtaga 960
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296 Pro Ser Arg Tyr Ile Ala Ile Ala Met Tyr Ser Ile Val Ile Cys Ile
297 20 25 30
299 Gly Leu Val Gly Asn Leu Leu Cys Ile Val Leu Val Lys Lys Arg
300 35 40 45
302 Lys Leu Arg Tyr Ser Ser Asp Val Tyr Phe Phe His Ala Ser Met Ala
303 50 55 60
305 Asp Leu Val Ser Thr Val Met Leu Pro Leu Trp Leu His Tyr Val Leu
306 65 70 75 80
308 Asn Phe Ala Gln Leu Ser Arg Gly Ala Cys Ile Ser Phe Ser Val Thr
309 85 90 95
311 Phe Tyr Val Pro Leu Phe Val Gln Ala Trp Leu Leu Ile Ser Ile Ala
312 100 105 110
314 Met Glu Arg Tyr Ser Asn Leu Val Trp Met Ala Pro Ile Ser Val Lys
315 115 120 125
317 Thr Ala Phe Lys His Cys Ile Gly Thr Trp Ile Val Ser Ala Phe Val
318 130 135 140
320 Ala Ser Pro Tyr Tyr Ala Tyr Arg Asn Ser His Asp Glu His Glu Cys
321 145 150 155 160
323 Ile Leu Gly Asn Tyr Thr Trp His Ile Asn Glu Pro Leu His Thr Cys
324 165 170 175
326 Met Asp Val Val Ile Ile Val Trp Thr Phe Leu Ala Pro Val Leu Val
327 180 185 190
329 Thr Ile Ile Ala Ser Val Lys Met Arg Arg Thr Thr Trp Gly Asn Thr

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